

WHAT IS CLAIMED IS:

1 1. A method of typing a growth arising in association with a congenital
2 melanocytic nevus, the method comprising providing a skin tumor sample from a patient and
3 detecting a change in chromosome number in a nucleic acid sample from the skin tumor
4 sample, wherein the change in chromosome number is selected from the group consisting of a
5 gain of chromosome 10, a gain of chromosome 11, a loss of chromosome 7, or a combination
6 thereof; thereby typing the skin tumor sample as a benign growth.

1 2. The method of claim 1, wherein the change in chromosome number is
2 a gain of chromosome 10.

1 3. The method of claim 1, wherein the change in chromosome number is
2 a gain of chromosome 11.

1 4. The method of claim 1, wherein the change in chromosome number is
2 a loss of chromosome 7.

1 5. The method of claim 1, further comprising detecting a gain or loss of
2 another chromosome.

1 6. The method of claim 1, wherein the detecting step comprises:
2 contacting a nucleic acid sample from the patient with a probe which
3 selectively hybridizes to a target polynucleotide sequence on a chromosome selected from the
4 group consisting of chromosome 10, chromosome 11, and chromosome 7; wherein the probe
5 is contacted with the sample under conditions in which the probe binds selectively with the
6 target polynucleotide sequence to form a stable hybridization complex;
7 detecting the formation of the hybridization complex; and
8 detecting a change in chromosome number, the change selected from the
9 group consisting of a gain of chromosome 10, a gain of chromosome 11 and a loss of
10 chromosome 7.

1 7. The method of claim 6, wherein the detecting step further comprises
2 amplifying the target nucleotide sequence.

1 8. The method of claim 7, wherein the target nucleotide sequence is
2 amplified using a polymerase chain reaction.

1 9. The method of claim 6, wherein the eprobe is a centromeric probe.

1 10. The method of claim 1, wherein the nucleic acid sample is an

2 interphase nucleus.

1 11. The method of claim 1, wherein the nucleic acid sample is a metaphase

2 cell.

1 12. The method of claim 6, wherein the probe is labeled with a fluorescent

2 label.

1 13. The method of claim 6, wherein the probe is labeled with digoxigenin

2 or biotin.

1 14. The method of claim 6, further comprising the step of blocking the

2 hybridization capacity of repetitive sequences in the nucleic acid sample.

1 15. The method of claim 14, wherein unlabeled blocking nucleic acids

2 comprising repetitive sequences are contacted with the sample.

1 16. The method of claim 15, wherein the unlabeled blocking nucleic acids

2 are Cot-1 DNA.

1 17. The method of claim 6, wherein the probe is bound to a solid substrate.

1 18. The method of claim 17, wherein the probe is a member of an array.